

RAW SEQUENCE LISTING DATE: 02/02/2001
 PATENT APPLICATION: US/09/165,460A TIME: 16:17:02

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TECH CENTER 1600/2800

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#5

3 <110> APPLICANT: Rine, Jasper
 4 Boyartchuk, Victor L
 5 Ashby, Matthew N
 7 <120> TITLE OF INVENTION: AFCL and RCE1: Isoprenylated CAAX Processing Enzymes
 9 <130> FILE REFERENCE: B96-006-3
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/165,460A
 C--> 12 <141> CURRENT FILING DATE: 1998-10-02
 14 <150> PRIOR APPLICATION NUMBER: 60/023,491
 15 <151> PRIOR FILING DATE: 1996-08-07
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1825
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Saccharomyces cerevisiae
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (343)..(1701)
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 35 aagaggcaat taaacttttc cctcttttcc taagtcattt actcaaaaac tetaattcct 180
 37 tcgtctctgt tctgccattt tctccagaaa aaaatcgacg ggaataaaa aaaaaaagac 240
 39 aacgaacaag agaaaaagt cgcgaattat aaaccacttc tataattaac aggaaaagga 300
 41 aggaaaaaaa aggaggaaat agaaaactgc aggcctttat tc atg ttt gat ctt 354
 42 Met Phe Asp Leu
 43 1
 45 aag acg att ctc gac cat cct aat atc ccg tgg aaa tta atc att tct 402
 46 Lys Thr Ile Leu Asp His Pro Asn Ile Pro Trp Lys Leu Ile Ile Ser
 47 5 10 15 20
 49 ggg ttc tgg att gcc caa ttt tct ttc gaa tct tac ttg acg tac aga 450
 50 Gly Phe Ser Ile Ala Gln Phe Ser Phe Glu Ser Tyr Leu Thr Tyr Arg
 51 25 30 35
 53 cag tac cag aag cta tct gaa aca aag ttg cca cct gtg ctg gaa gac 498
 54 Gln Tyr Gln Lys Leu Ser Glu Thr Lys Leu Pro Pro Val Leu Glu Asp
 55 40 45 50
 57 gaa att gat gat gaa act ttt cat aaa tca agg aac tac tcc cgg gcc 546
 58 Glu Ile Asp Asp Glu Thr Phe His Lys Ser Arg Asn Tyr Ser Arg Ala
 59 55 60 65
 61 aag gcc aag ttc tcc att ttc ggt gac gtc tat aac cta gcc caa aag 594
 62 Lys Ala Lys Phe Ser Ile Phe Gly Asp Val Tyr Asn Leu Ala Gln Lys
 63 70 75 80
 65 cta gtt ttc atc aaa tac gac ctc ttc cct aaa atc tgg cac atg gcc 642
 66 Leu Val Phe Ile Lys Tyr Asp Leu Phe Pro Lys Ile Trp His Met Ala
 67 85 90 95 100
 69 gtt tct tta ttg aat gca gtc ctg cca gtc aga ttt cat atg gtc tcc 690
 70 Val Ser Leu Leu Asn Ala Val Leu Pro Val Arg Phe His Met Val Ser

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73 act gtc gca cag agt tta tgc ttc ttg ggt ctc tta tcc agt ttg tct 738
74 Thr Val Ala Gln Ser Leu Cys Phe Leu Gly Leu Leu Ser Ser Leu Ser
75          120          125          130
77 acc ttg gtt gat ttg cca ctc tct tac tat agc cat ttt gtc ctg gaa 786
78 Thr Leu Val Asp Leu Pro Leu Ser Tyr Tyr Ser His Phe Val Leu Gln
79          135          140          145
81 gaa aaa ttt ggt ttc aat aaa ttg acc gtc caa cta tgg atc acc gat 834
82 Glu Lys Phe Gly Phe Asn Lys Leu Thr Val Gln Leu Trp Ile Thr Asp
83          150          155          160
85 atg atc aag agt ctg act ttg gcg tat gct att ggt ggc cca atc ctt 882
86 Met Ile Lys Ser Leu Thr Leu Ala Tyr Ala Ile Gly Gly Pro Ile Leu
87 165          170          175          180
89 tac ctg ttc ctt aag atc ttt gat aaa ttc cct act gat ttc ctt tgg 930
90 Tyr Leu Phe Leu Lys Ile Phe Asp Lys Phe Pro Thr Asp Phe Leu Trp
91          185          190          195
93 tac att atg gtc ttc ttg ttc gtt gtc caa atc tta gcc atg aca atc 978
94 Tyr Ile Met Val Phe Leu Phe Val Val Gln Ile Leu Ala Met Thr Ile
95          200          205          210
97 att cca gtc ttc atc atg ccc atg ttt aat aag ttc act cca ttg gaq 1026
98 Ile Pro Val Phe Ile Met Pro Met Phe Asn Lys Phe Thr Pro Leu Glu
99          215          220          225
101 gac ggt gaa ctg aaa aaa tct att gaa agt ttg gcc gat aga gtt ggg 1074
102 Asp Gly Glu Leu Lys Lys Ser Ile Glu Ser Leu Ala Asp Arg Val Gly
103          230          235          240
105 ttc cct cta gat aag att ttt gtc att gac ggc tca aaa aga tct tct 1122
106 Phe Pro Leu Asp Lys Ile Phe Val Ile Asp Gly Ser Lys Arg Ser Ser
107 245          250          255          260
109 cat tca aac gca tat ttc aca ggt ttg cca ttc acc tcc aag aga att 1170
110 His Ser Asn Ala Tyr Phe Thr Gly Leu Pro Phe Thr Ser Lys Arg Ile
111          265          270          275
113 gtt ttg ttc gac act tta gtg aac agt aat tct act gat gaa att acg 1218
114 Val Leu Phe Asp Thr Leu Val Asn Ser Asn Ser Thr Asp Glu Ile Thr
115          280          285          290
117 gct gtt ttg gcc cat gaa atc ggt cac tgg caa aaa aac cac atc gtt 1266
118 Ala Val Leu Ala His Glu Ile Gly His Trp Gln Lys Asn His Ile Val
119          295          300          305
121 aat atg gtc atc ttt agt caa ttg cac acc ttc ctc att ttc tcc ctt 1314
122 Asn Met Val Ile Phe Ser Gln Leu His Thr Phe Leu Ile Phe Ser Leu
123          310          315          320
125 ttc acc agc atc tac aga aat aca tca ttt tac aac acc ttc ggc ttt 1362
126 Phe Thr Ser Ile Tyr Arg Asn Thr Ser Phe Tyr Asn Thr Phe Gly Phe
127 325          330          335          340
129 ttc tta gag aag tcc act ggc agt ttt gtt gat ccc gtt atc act aag 1410
130 Phe Leu Glu Lys Ser Thr Gly Ser Phe Val Asp Pro Val Ile Thr Lys
131          345          350          355
133 gaa ttc ccc att atc att gga ttt atg tta ttt aac gac tta tta act 1458
134 Glu Phe Pro Ile Ile Ile Gly Phe Met Leu Phe Asn Asp Leu Leu Thr
135          360          365          370

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138 Pro Leu Glu Cys Ala Met Gln Phe Val Met Ser Leu Ile Ser Arg Thr
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142 His Glu Tyr Gln Ala Asp Ala Tyr Ala Lys Lys Leu Gly Tyr Lys Glu
143      390      395      400
145 aat cta tgt agg gct cta att gat cta caa atc aaa aac ctt tcc acc 1602
146 Asn Leu Cys Arg Ala Leu Ile Asp Leu Gln Ile Lys Asn Leu Ser Thr
147 405      410      415      420
149 atg aat gta gat cct ctg tat tct agc tat cat tat tcc cat cca act 1650
150 Met Asn Val Asp Pro Leu Tyr Ser Ser Tyr His Tyr Ser His Pro Thr
151      425      430      435
153 cta gct gaa aga tgc acc gct cta gac tat gtt agt gaa aag aag aaa 1698
154 Leu Ala Glu Arg Ser Thr Ala Leu Asp Tyr Val Ser Glu Lys Lys Lys
155      440      445      450
157 aac taatctatag agtacacata ttagcatgta ccgttaaatt cagcttcggt 1751
158 Asn
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162 aacgattaaa catt 1825
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178 35 40 45
180 Val Leu Glu Asp Glu Ile Asp Asp Glu Thr Phe His Lys Ser Arg Asn
181 50 55 60
183 Tyr Ser Arg Ala Lys Ala Lys Phe Ser Ile Phe Gly Asp Val Tyr Asn
184 65 70 75 80
186 Leu Ala Gln Lys Leu Val Phe Ile Lys Tyr Asp Leu Phe Pro Lys Ile
187 85 90 95
189 Trp His Met Ala Val Ser Leu Leu Asn Ala Val Leu Pro Val Arg Phe
190 100 105 110
192 His Met Val Ser Thr Val Ala Gln Ser Leu Cys Phe Leu Gly Leu Leu
193 115 120 125
195 Ser Ser Leu Ser Thr Leu Val Asp Leu Pro Leu Ser Tyr Tyr Ser His
196 130 135 140
198 Phe Val Leu Glu Glu Lys Phe Gly Phe Asn Lys Leu Thr Val Gln Leu
199 145 150 155 160
201 Trp Ile Thr Asp Met Ile Lys Ser Leu Thr Leu Ala Tyr Ala Ile Gly
202 165 170 175
204 Gly Pro Ile Leu Tyr Leu Phe Leu Lys Ile Phe Asp Lys Phe Pro Thr
205 180 185 190
207 Asp Phe Leu Trp Tyr Ile Met Val Phe Leu Phe Val Val Gln Ile Leu

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210 Ala Met Thr Ile Ile Pro Val Phe Ile Met Pro Met Phe Asn Lys Phe
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214 225          230          235          240
216 Asp Arg Val Gly Phe Pro Leu Asp Lys Ile Phe Val Ile Asp Gly Ser
217          245          250          255
219 Lys Arg Ser Ser His Ser Asn Ala Tyr Phe Thr Gly Leu Pro Phe Thr
220          260          265          270
222 Ser Lys Arg Ile Val Leu Phe Asp Thr Leu Val Asn Ser Asn Ser Thr
223          275          280          285
225 Asp Glu Ile Thr Ala Val Leu Ala His Glu Ile Gly His Trp Gln Lys
226          290          295          300
228 Asn His Ile Val Asn Met Val Ile Phe Ser Gln Leu His Thr Phe Leu
229 305          310          315          320
231 Ile Phe Ser Leu Phe Thr Ser Ile Tyr Arg Asn Thr Ser Phe Tyr Asn
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234 Thr Phe Gly Phe Phe Leu Glu Lys Ser Thr Gly Ser Phe Val Asp Pro
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237 Val Ile Thr Lys Glu Phe Pro Ile Ile Ile Gly Phe Met Leu Phe Asn
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241          370          375          380
243 Ile Ser Arg Thr His Glu Tyr Gln Ala Asp Ala Tyr Ala Lys Lys Leu
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246 Gly Tyr Lys Gln Asn Leu Cys Arg Ala Leu Ile Asp Leu Gln Ile Lys
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249 Asn Leu Ser Thr Met Asn Val Asp Pro Leu Tyr Ser Ser Tyr His Tyr
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274 atataatatg aataggggag accgtaggcc aaagggaactg aaatttacag attttattac 180
276 ttcacagctg tttaacgata tcgaaagcat ttgcaacttg aaagttagtg ttcaacaactt 240
278 atccaacatt tttaaaaaac aggtcagtag cctaaaaaca caetcaaaag acgcattatc 300
280 tgaggattca atatcgacac caggtaacgg tagttcatcg tcgccaggtt cagcgtcatt 360
282 aacgccagta accttttcat ccaagagtag tttattttta cctagcggta gctcgtctac 420
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286 caaacgagac attaatgtga acttgggaatt taataaggagc attaaggaaa ctttaattcc 540
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290 aaaccatctt ggcgtagcga agattgatat ccttatttct qitagcaag tgacaaaata 660
292 aaaaaacatt agaaaaaatt ctcgttactt ttottataga tatagatata tgtatggttt 720
294 gcttatagat gaaggtatctt ategcgtcct ttgtattccc tattattaat aaaattcttt 780
296 taaaaatgcat tttctgggtgc tcttttgttg cttctgtatt tttttttttt tggaccactg 840
298 gatggaaaac ctttgatgat ttattacctt ttattttaag ttactaaaat atcgagattt 900
300 caggaaacaaa acatagaatt ttctttgtca agaaaaataa aacgaataa attgatgctt 960
302 tgactactga ctgtctgtca tagagagaac cagaacagca atg cta caa ttc tca 1015
303                                     Met Leu Gln Phe Ser
304                                     1 5
306 aca ttt cta gtg ctc cta tac atc tcc ata tcc tat gtg cta ccg cta 1063
307 Thr Phe Leu Val Leu Leu Tyr Ile Ser Ile Ser Tyr Val Leu Pro Leu
308                                     10 15 20
310 tat gca act tca caa cca gaa ggg tct aaa cga gat aat cct cga acg 1111
311 Tyr Ala Thr Ser Gln Pro Glu Gly Ser Lys Arg Asp Asn Pro Arg Thr
312                                     25 30 35
314 att aaa tct cgc atg caa aaa ctt aca att atg cta att tcc aac ctt 1159
315 Ile Lys Ser Arg Met Gln Lys Leu Thr Ile Met Leu Ile Ser Asn Leu
316                                     40 45 50
318 ttt ttg gtg cct ttt tta caa tct caa tta tct agt acc act tca cat 1207
319 Phe Leu Val Pro Phe Leu Gln Ser Gln Leu Ser Ser Thr Thr Ser His
320                                     55 60 65
322 ata agt ttc aag gac gca ttt tta ggc tta ggt att atc cca ggt tat 1255
323 Ile Ser Phe Lys Asp Ala Phe Leu Gly Leu Gly Ile Ile Pro Gly Tyr
324 70 75 80 85
326 tac gct gca ttg cca aac cct tgg caa ttc agc cag ttc gtg aaa gac 1303
327 Tyr Ala Ala Leu Pro Asn Pro Trp Gln Phe Ser Gln Phe Val Lys Asp
328                                     90 95 100
330 tta acg aaa tgt ctt gcg atg tta ttg acc tta tat tgt gga ccc gtt 1351
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332                                     105 110 115
334 tta gat ttt gta tta tat cat tta aat cca aag agc tct ata ctt 1399
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336                                     120 125 130
338 gaa gat ttt tac cat gaa ttc ctg aat att tgg agt ttc agg aat ttt 1447
339 Glu Asp Phe Tyr His Glu Phe Leu Asn Ile Trp Ser Phe Arg Asn Phe
340                                     135 140 145
342 ata ttt gca cca ata act gag gaa ata ttt tac acg tca atg ctt ttg 1495
343 Ile Phe Ala Pro Ile Thr Glu Glu Ile Phe Tyr Thr Ser Met Leu Leu
344 150 155 160 165
346 act acg tac tta aac cta ata ccg cat tcg caa cta agc tat caa cag 1543
347 Thr Thr Tyr Leu Asn Leu Ile Pro His Ser Gln Leu Ser Tyr Gln Gln
348                                     170 175 180
350 tta ttt tgg caa cca tcg ctt ttt ttt gga ctt gcg cac gca cac cat 1591
351 Leu Phe Trp Gln Pro Ser Leu Phe Phe Gly Leu Ala His Ala His His
352                                     185 190 195
354 gct tat gag caa tta cag gaa ggc tcc atg aca act gtt tcc att ctg 1639
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VERIFICATION SUMMARY DATE: 02/02/2001
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date